

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/800,909DATE: 05/05/2001
TIME: 00:04:28

INPUT SET: S36630.raw

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This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANT: WALLACH, David
BIGDA, Jacek
BELETSKY, Igor
METT, Igor
ENGELMANN, Hartmut

ENTERED

(ii) TITLE OF INVENTION: TNF INHIBITORS

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BROWDY AND NEIMARK
(B) STREET: 419 Seventh Street, N.W.
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/800,909
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/476,862
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: IL 94039
(B) FILING DATE: 06-APR-1990

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: IL 91229
(B) FILING DATE: 06-AUG-1989

(vii) PRIOR APPLICATION DATA:

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47 (A) APPLICATION NUMBER: IL 90339
48 (B) FILING DATE: 18-MAY-1989
49
50 (viii) ATTORNEY/AGENT INFORMATION:
51 (A) NAME: BROWDY, Roger L.
52 (B) REGISTRATION NUMBER: 25,618
53 (C) REFERENCE/DOCKET NUMBER: WALLACH=12A
54
55 (ix) TELECOMMUNICATION INFORMATION:
56 (A) TELEPHONE: 202-628-5197
57 (B) TELEFAX: 202-737-3528
58
59
60 (2) INFORMATION FOR SEQ ID NO:1:
61
62 (i) SEQUENCE CHARACTERISTICS:
63 (A) LENGTH: 2224 base pairs
64 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: single
66 (D) TOPOLOGY: linear
67
68 (ii) MOLECULE TYPE: cDNA
69
70 (ix) FEATURE:
71 (A) NAME/KEY: CDS
72 (B) LOCATION: 90..1472
73
74
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
76
77 GCGAGCGCAG CGGAGCCTGG AGAGAAGGCG CTGGGCTGCG AGGGCGCGAG GGCGCGAGGG 60
78
79 CAGGGGGCAA CCGGACCCCG CCCGCACCC ATG GCG CCC GTC GCC GTC TGG GCC 113
80 Met Ala Pro Val Ala Val Trp Ala
81 1 5
82
83 GCG CTG, GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC 161
84 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
85 10 15 20
86
87 GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC 209
88 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
89 25 30 35 40
90
91 CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA 257
92 Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
93 45 50 55
94
95 TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC 305
96 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
97 60 65 70
98
99 ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC 353

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100	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	Thr	Gln	Leu	Trp	Asn	
101			75					80					85				
102																	
103	TGG	GTT	CCC	GAG	TGC	TTG	AGC	TGT	GGC	TCC	CGC	TGT	AGC	TCT	GAC	CAG	401
104	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	
105		90					95					100					
106																	
107	GTG	GAA	ACT	CAA	GCC	TGC	ACT	CGG	GAA	CAG	AAC	CGC	ATC	TGC	ACC	TGC	449
108	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys	
109	105					110					115					120	
110																	
111	AGG	CCC	GGC	TGG	TAC	TGC	GCG	CTG	AGC	AAG	CAG	GAG	GGG	TGC	CGG	CTG	497
112	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	
113					125					130					135		
114																	
115	TGC	GCG	CCG	CTG	CGC	AAG	TGC	CGC	CCG	GGC	TTC	GGC	GTG	GCC	AGA	CCA	545
116	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	
117				140					145					150			
118																	
119	GGA	ACT	GAA	ACA	TCA	GAC	GTG	GTG	TGC	AAG	CCC	TGT	GCC	CCG	GGG	ACG	593
120	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	
121			155					160					165				
122																	
123	TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG	CCC	CAC	CAG	ATC	641
124	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
125		170					175					180					
126																	
127	TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	689
128	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	
129	185					190					195				200		
130																	
131	ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	737
132	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
133					205					210					215		
134																	
135	CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	785
136	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
137				220				225					230				
138																	
139	CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	833
140	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
141			235					240					245				
142																	
143	CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	881
144	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
145		250					255					260					
146																	
147	ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	929
148	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
149	265					270					275					280	
150																	
151	TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	977
152	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	

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	285	290	295	
153				
154				
155	GAA GCC AAG GTG CCT CAC TTG CCT GCC GAT AAG GCC CGG GGT ACA CAG			1025
156	Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln			
157	300	305	310	
158				
159	GGC CCC GAG CAG CAG CAC CTG CTG ATC ACA GCG CCG AGC TCC AGC AGC			1073
160	Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser			
161	315	320	325	
162				
163	AGC TCC CTG GAG AGC TCG GCC AGT GCG TTG GAC AGA AGG GCG CCC ACT			1121
164	Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr			
165	330	335	340	
166				
167	CGG AAC CAG CCA CAG GCA CCA GGC GTG GAG GCC AGT GGG GCC GGG GAG			1169
168	Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu			
169	345	350	355	360
170				
171	GCC CGG GCC AGC ACC GGG AGC TCA GAT TCT TCC CCT GGT GGC CAT GGG			1217
172	Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly			
173	365	370	375	
174				
175	ACC CAG GTC AAT GTC ACC TGC ATC GTG AAC GTC TGT AGC AGC TCT GAC			1265
176	Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp			
177	380	385	390	
178				
179	CAC AGC TCA CAG TGC TCC TCC CAA GCC AGC TCC ACA ATG GGA GAC ACA			1313
180	His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr			
181	395	400	405	
182				
183	GAT TCC AGC CCC TCG GAG TCC CCG AAG GAC GAG CAG GTC CCC TTC TCC			1361
184	Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser			
185	410	415	420	
186				
187	AAG GAG GAA TGT GCC TTT CGG TCA CAG CTG GAG ACG CCA GAG ACC CTG			1409
188	Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu			
189	425	430	435	440
190				
191	CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC CTT GGA GTG CCT GAT GCT			1457
192	Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala			
193	445	450	455	
194				
195	GGG ATG AAG CCC AGT TAACCAGGCC GGTGTGGGCT GTGTCGTAGC CAAGGTGGGC			1512
196	Gly Met Lys Pro Ser			
197	460			
198				
199	TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCCC CCACCACTAG			1572
200				
201	GA CTCTGAGG CTCTTTCTGG GCCAAGTTCC TCTAGTGCCC TCCACAGCCG CAGCCTCCCT			1632
202				
203	CTGACCTGCA GGCCAAGAGC AGAGGCAGCG AGTTGGGGAA AGCCTCTGCT GCCATGGTGT			1692
204				
205	GTCCCTCTCG GAAGGCTGGC TGGGCATGGA CGTTCGGGGC ATGCTGGGGC AAGTCCCTGA			1752

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206
207 CTCTCTGTGA CCTGCCCCGC CCAGCTGCAC CTGCCAGCCT GGCTTCTGGA GCCCTTGGGT 1812
208
209 TTTTGTGTTG TTTGTTTGTT TGTGTTGTTG TTTCTCCCCC TGGGCTCTGC CCAGCTCTGG 1872
210
211 CTTCCAGAAA ACCCCAGCAT CCTTTTCTGC AGAGGGGCTT TCTGGAGAGG AGGGATGCTG 1932
212
213 CCTGAGTCAC CCATGAAGAC AGGACAGTGC TTCAGCCTGA GGCTGAGACT GCGGGATGGT 1992
214
215 CCTGGGGCTC TGTGTAGGGA GGAGGTGGCA GCCCTGTAGG GAACGGGGTC CTTCAAGTTA 2052
216
217 GCTCAGGAGG CTTGGAAAGC ATCACCTCAG GCCAGGTGCA GTGGCTCACG CCTATGATCC 2112
218
219 CAGCACTTTG GGAGGCTGAG GCGGGTGGAT CACCTGAGGT TAGGAGTTCG AGACCAGCCT 2172
220
221 GGCCAACATG GTAAAACCCC ATCTCTACTA AAAATACAGA AATTAGCCGG GC 2224
222
223
224 (2) INFORMATION FOR SEQ ID NO:2:
225
226 (i) SEQUENCE CHARACTERISTICS:
227 (A) LENGTH: 461 amino acids
228 (B) TYPE: amino acid
229 (D) TOPOLOGY: linear
230
231 (ii) MOLECULE TYPE: protein
232
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
234
235 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
236 1 5 10 15
237
238 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
239 20 25 30
240
241 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
242 35 40 45
243
244 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
245 50 55 60
246
247 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
248 65 70 75 80
249
250 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
251 85 90 95
252
253 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
254 100 105 110
255
256 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
257 115 120 125
258

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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